

FIG. 1

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graph TD
    A[CRUDE RECOMBINANT HUMAN LACTOFERRIN (FERMENTATION BROTH)] --> B[BUFFER EXCHANGE/CONCENTRATION]
    B -- CONCENTRATE --> C[BLUE SEPHAROSE CL-6B]
    C --> D[CONTROL PORE GLASS (CPG)]
    D --> E[BUFFER EXCHANGE/CONCENTRATION]
    E --> F[T-GEL]
    E -- CONCENTRATE --> G[IDA Ni++]
    E --> H[PHENYL SEPHAROSE]
  
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FIG. 2

1	GGATCCGGCCGTAGGAGAAGGAGTGTTCAGTGGTGCGCCGTATCCCAACCCGAGGCCACA -----+-----+-----+-----+-----+ CCTAGGCCGGCATCCTCTTCCTCACAAGTCACCACGCGGCATAGGGTTGGGCTCCGGTGT GlySerGlyArgArgArgArgSerValGlnTrpCysAlaValSerGlnProGluAlaThr	60
61	AAATGCTTCCAATGGCAAAGGAATATGAGAAAAGTGGTGGCCCTCCTGTCAGCTGCATA -----+-----+-----+-----+-----+ TTTACGAAGGTTACCGTTTCCTTATACTCTTTTCACGCACCGGGAGGACAGTCCGACGTAT LysCysPheGlnTrpGlnArgAsnMetArgLysValArgGlyProProValSerCysIle	120
121	AAGAGAGACTCCCCCATCCAGTGTATCCAGGCCATTGCGGAAAACAGGGCCGATGCTGTG -----+-----+-----+-----+-----+ TTCTCTCTGAGGGGGTAGGTACATAGGTCCGGTAACGCCTTTTGTCCCGGCTACGACAC LysArgAspSerProIleGlnCysIleGlnAlaIleAlaGluAsnArgAlaAspAlaVal	180
181	ACCCCTTGATGGTGGTTTCATATACGAGGCAGGCCCTGGCCCCCTACAACTGCGACCTGTA -----+-----+-----+-----+-----+ TGGGAACTACCACCAAAGTATATGCTCCGTCCGGACCGGGGGATGTTTGACGCTGGACAT ThrLeuAspGlyGlyPheIleTyrGluAlaGlyLeuAlaProTyrLysLeuArgProVal	240
241	GCGGCGGAAGTCTACGGGACCGAAAAGACAGCCACGAACTCACTATTATGCCGTGGCTGTG -----+-----+-----+-----+-----+ CGCCGCCTTCAGATGCCCTGGCTTTCTGTCCGTGCTTGAGTGATAATACGGCACCCACAC AlaAlaGluValTyrGlyThrGluArgGlnProArgThrHisTyrTyrAlaValAlaVal	300
301	GTGAAGAAGGGCGGCAGcTTTCAGCTGAACGAACTGCAAGGTCTGAAGTCTGCCACACA -----+-----+-----+-----+-----+ CACTTCTTCCCGCCGTCgAAAGTCGACTTGCTTGACGTTCCAGACTTCAGGACGGTGTGT ValLysLysGlyGlySerPheGlnLeuAsnGluLeuGlnGlyLeuLysSerCysHisThr	360
361	GGCCTTCGCAGGACCGCTGGATGGAATGTCCCTATAGGGACACTTCGTCCATTCTTGAAT -----+-----+-----+-----+-----+ CCGGAGCGTCTCGCGACCTACCTTACAGGGATATCCCTGTGAAGCAGGTAAGAACTTA GlyLeuArgArgThrAlaGlyTrpAsnValProIleGlyThrLeuArgProPheLeuAsn	420
421	TGGACGGGTCCACCTGAGCCCATTGAGGCAGCTGTGGCCAGGTTCTTCTCAGCCAGCTGT -----+-----+-----+-----+-----+ ACCTGCCCAGGTGGACTCGGGTAACTCCGTCCGACACCGGTCCAAGAAGAGTCGGTCCGACA TrpThrGlyProProGluProIleGluAlaAlaValAlaArgPhePheSerAlaSerCys	480
481	GTTCCCGGTGCAGATAAAGGACAGTTCCCCAACCTGTGTGCGCTGTGTGCGGGGACAGGG -----+-----+-----+-----+-----+ CAAGGGCCACGTCTATTTCTGTCAAGGGGTTGGACACAGCGGACACAGCCCCCTGTCCC ValProGlyAlaAspLysGlyGlnPheProAsnLeuCysArgLeuCysAlaGlyThrGly	540
541	GAAAACAAATGTGCCTTCTCCTCCCAGGAACCGTACTTCAGCTACTCTGGTGCCTTCAAG -----+-----+-----+-----+-----+ CTTTTGTTTACACGGAAGAGGAGGGTCCTTGGCATGAAGTCGATGAGACCACGGAAGTTC GluAsnLysCysAlaPheSerSerGlnGluProTyrPheSerTyrSerGlyAlaPheLys	600

FIG. 3a

601	TGTCTGAGAGACGGGGCTGGAGACCTGGCTTTTATCAGAGAGAGCACAGTGTTCGAGGAC -----+-----+-----+-----+-----+-----+-----+-----+ ACAGACTCTCTGCCCCGACCTCTGCACCGAAAAATAGTCTCTCTCGTGTCAAACTCCTG CysLeuArgAspGlyAlaGlyAspValAlaPheIleArgGluSerThrValPheGluAsp	660
661	CTGTCAGACGAGGCTGAAAGGGACGAGTATGAGTTACTCTGCCCAGACAACACTCGGAAG -----+-----+-----+-----+-----+-----+-----+-----+ GACAGTCTGCTCCGACTTTCCTGCTCATACTCAATGAGACGGGTCTGTTCTGAGCCTTC LeuSerAspGluAlaGluArgAspGluTyrGluLeuLeuCysProAspAsnThrArgLys	720
721	CCAGTGGACAAGTTCAAAGACTGCCATCTGGCCCCGGTCCCTTCTCATGCCGTTGTGGCA -----+-----+-----+-----+-----+-----+-----+-----+ GGTCACCTGTTCAAGTTTCTGACGGTAGACCGGGCCCAGGGAAGAGTACGGCAACACCGT ProValAspLysPheLysAspCysHisLeuAlaArgValProSerHisAlaValValAla	780
781	CGAAGTGTGAATGGCAAGGAGGATGCCATCTGGAATCTTCTCCGCCAGGCACAGGAAAAAG -----+-----+-----+-----+-----+-----+-----+-----+ GCTTCACACTTACCGTTCCTCCTACGGTAGACCTTAGAAGAGGCGGTCCGTGTCTTTTC ArgSerValAsnGlyLysGluAspAlaIleTrpAsnLeuLeuArgGlnAlaGlnGluLys	840
841	TTTGAAAGGACAAGTCAACGAAATTCAGCTCTTTGGCTCCCCTAGTGGGCAGAAAGAT -----+-----+-----+-----+-----+-----+-----+-----+ AAACCTTTCTCTGTTCAAGTGGCTTTAAGGTCCAGAAACCGAGGGGATCACCCGTCTTTCTA PheGlyLysAspLysSerProLysPheGlnLeuPheGlySerProSerGlyGlnLysAsp	900
901	CTGCTGTTCAAGGACTCTGCCATTGGGTTTTCGAGGGTGCCCCCGAGGATAGATTCTGGG -----+-----+-----+-----+-----+-----+-----+-----+ GACGACAAGTTCCTGAGACGGTAACCCAAAAGCTCCCACGGGGGCTCCTATCTAAGACCC LeuLeuPheLysAspSerAlaIleGlyPheSerArgValProProArgIleAspSerGly	960
961	CTGTACCTTGGCTCCGGCTACTTCACTGCCATCCAGAACTTGAGGAAAAGTGAGGAGGAA -----+-----+-----+-----+-----+-----+-----+-----+ GACATGGAACCGAGGCCGATGAAGTGACGGTAGGTCTTGAACCTCCTTTTCACTCCTCCTT LeuTyrLeuGlySerGlyTyrPheThrAlaIleGlnAsnLeuArgLysSerGluGluGlu	1020
1021	GTGGCTGCCCCGGCTGCGCGGGTCTGTGGTGTGCGGTGGGCGAGCAGGAGCTGCGCAAG -----+-----+-----+-----+-----+-----+-----+-----+ CACCGACGGGGCCGACGCGCCAGCACACCACACGCCACCCGCTCGTCTCTGACGCGTTC ValAlaAlaArgArgAlaArgValValTrpCysAlaValGlyGluGlnGluLeuArgLys	1080
1081	TGTAACCAGTGGAGTGGCTTGAGCGAAGGCAGCGTGACCTGCTCCTCGGCCTCCACCACA -----+-----+-----+-----+-----+-----+-----+-----+ ACATTGGTCACTCACCAGAACTCGCTTCCGTCCGACTGGACGAGGAGCCCGAGGTGGTGT CysAsnGlnTrpSerGlyLeuSerGluGlySerValThrCysSerSerAlaSerThrThr	1140
1141	GAGGACTGCATCGCCCTGGTGCTGAAAGGAGAAGCTGATGCCATGAGTTTGGATGGAGGA -----+-----+-----+-----+-----+-----+-----+-----+ CTCCTGACGTAGCGGGACCACGACTTTCCTCTCGACTACGGTACTCAAACCTACCTCCT GluAspCysIleAlaLeuValLeuLysGlyGluAlaAspAlaMetSerLeuAspGlyGly	1200

FIG. 3b

1201	TATGTGTACACTGCAGGCAAATGTGGTTTGGTGCCTGTCTGGCAGAGAACTACAAATCC -----+-----+-----+-----+-----+-----+ ATACACATGTGACGTCCGTTTACACCAAACCGGACAGGACCGTCTCTTGATGTTTAGG TyrValTyrThrAlaGlyLysCysGlyLeuValProValLeuAlaGluAsnTyrLysSer	1260
1261	CAACAAAGCAGTGACCCTGATCCTAACTGTGTGGATAGACCTGTGGAAGGATATCTTGCT -----+-----+-----+-----+-----+-----+ GTTGTTTCGTCACTGGGACTAGGATTGACACACCTATCTGGACACCTTCCTATAGAACGA GlnGlnSerSerAspProAspProAsnCysValAspArgProValGluGlyTyrLeuAla	1320
1321	GTGGCGGTGGTTAGGAGATCAGACACTAGCCTTACCTGGAACCTCTGTGAAAGGCAAGAAG -----+-----+-----+-----+-----+-----+ CACCGCCACCAATCCTCTAGTCTGTGATCGGAATGGACCTTGAGACACTTTCCGTTCTTC ValAlaValValArgArgSerAspThrSerLeuThrTrpAsnSerValLysGlyLysLys	1380
1381	TCCTGCCACACCGCCGTGGACAGGACTGCAGGCTGGAATATCCCCATGGGCGCTGCTCTTC -----+-----+-----+-----+-----+-----+ AGGACGGTGTGGCGGCACCTGTCTGACGTCCGACCTTATAGGGGTACCCGGACGAGAAG SerCysHisThrAlaValAspArgThrAlaGlyTrpAsnIleProMetGlyLeuLeuPhe	1440
1441	AACCAGACGGGCTCCTGCAAATTTGATGAATATTTCACTCAAAGCTGTGCCCCCTGGGTCT -----+-----+-----+-----+-----+-----+ TTGGTCTGCCCCGAGGACGTTTAACTACTTATAAAGTCAGTTTCGACACGGGGACCCAGA AsnGlnThrGlySerCysLysPheAspGluTyrPheSerGlnSerCysAlaProGlySer	1500
1501	GACCCGAGATCTAATCTCTGTGCTCTGTGTATTGGCGACGAGCAGGGTGAGAATAAGTGC -----+-----+-----+-----+-----+-----+ CTGGGCTCTAGATTAGAGACACGAGACACATAACCGCTGCTCGTCCCACTCTTATTCACG AspProArgSerAsnLeuCysAlaLeuCysIleGlyAspGluGlnGlyGluAsnLysCys	1560
1561	GTGCCCCAACAGCAACGAGAGATACTACGGCTACACTGGGGCTTTCCGGTGCCTGGCTGAG -----+-----+-----+-----+-----+-----+ CACGGGTTGTCGTTGCTCTCTATGATGCCGATGTGACCCCGAAAGGCCACGGACCGACTC ValProAsnSerAsnGluArgTyrTyrGlyTyrThrGlyAlaPheArgCysLeuAlaGlu	1620
1621	AATGCTGGAGACGTTGCATTTGTGAAAGATGTCACTGTCTTGACAGAACTGATGGAAAT -----+-----+-----+-----+-----+-----+ TTACGACCTCTGCAACGTAAACACTTTCTACAGTGACAGAACGTCTTGACTACCTTTA AsnAlaGlyAspValAlaPheValLysAspValThrValLeuGlnAsnThrAspGlyAsn	1680
1681	AACAATGAGGCATGGGCTAAGGATTTGAAGCTGGCAGACTTTGCGCTGCTGTGCCTCGAT -----+-----+-----+-----+-----+-----+ TTGTTACTCCGTACCCGATTCTTAACTTCGACCGTCTGAAACCGGACGACACGGAGCTA AsnAsnGluAlaTrpAlaLysAspLeuLysLeuAlaAspPheAlaLeuLeuCysLeuAsp	1740
1741	GGCAAACGGAAGCCTGTGACTGAGGCTAGAAGCTGCCATCTTGCCATGGCCCCGAATCAT -----+-----+-----+-----+-----+-----+ CCGTTTTCCTTCGGACACTGACTCCGATCTTCGACGGTAGAACGGTACCGGGGCTTAGTA GlyLysArgLysProValThrGluAlaArgSerCysHisLeuAlaMetAlaProAsnHis	1800

FIG. 3c

1801	GCCGTGGTGTCTCGGATGGATAAGGTGGAACGCCTGAAACAGGTGTTGCTCCACCAACAG -----+-----+-----+-----+-----+-----+-----+-----+ CGGCACCACAGAGCCTACCTATTCCACCTTGGGACTTTGTCCACAACGAGGTGTTGTGTC AlaValValSerArgMetAspLysValGluArgLeuLysGlnValLeuLeuHisGlnGln	1860
1861	GCTAAATTTGGGAGAAATGGATCTGACTGCCCGGACAAGTTTTGCTTATTCCAGTCTGAA -----+-----+-----+-----+-----+-----+-----+-----+ CGATTTAAACCCTCTTTACCTAGACTGACGGGCCTGTTCAAAACGAATAAGGTCAGACTT AlaLysPheGlyArgAsnGlySerAspCysProAspLysPheCysLeuPheGlnSerGlu	1920
1921	ACCAAAAACCTTCTGTTCAATGACAACACTGAGTGTCTGGCCAGACTCCATGGCAAAAACA -----+-----+-----+-----+-----+-----+-----+-----+ TGGTTTTTGAAGACAAGTTACTGTTGTGACTCACAGACCGGTCTGAGGTACCGTTTTGT ThrLysAsnLeuLeuPheAsnAspAsnThrGluCysLeuAlaArgLeuHisGlyLysThr	1980
1981	ACATATGAAAAATATTTGGGACCACAGTATGTGCGAGGCATTACTAATCTGAAAAAGTGC -----+-----+-----+-----+-----+-----+-----+-----+ TGTATACTTTTTATAAACCCCTGGTGTCTATACAGCGTCCGTAATGATTAGACTTTTTTCAGC ThrTyrGluLysTyrLeuGlyProGlnTyrValAlaGlyIleThrAsnLeuLysLysCys	2040
2041	TCAACCTCCCCCCTCCTGGAAGCCTGTGAATTCCTCAGGAAGTAA -----+-----+-----+-----+-----+-----+-----+-----+ AGTTGGAGGGGGGAGGACCTTCGGACACTTAAGGAGTCCTTCATTT SerThrSerProLeuLeuGluAlaCysGluPheLeuArgLysEnd	2086

FIG. 3d

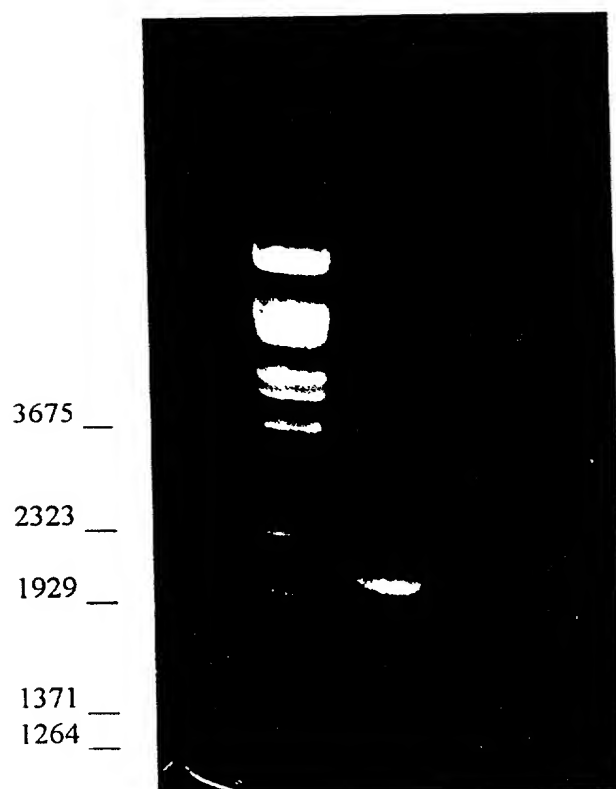


FIG. 4

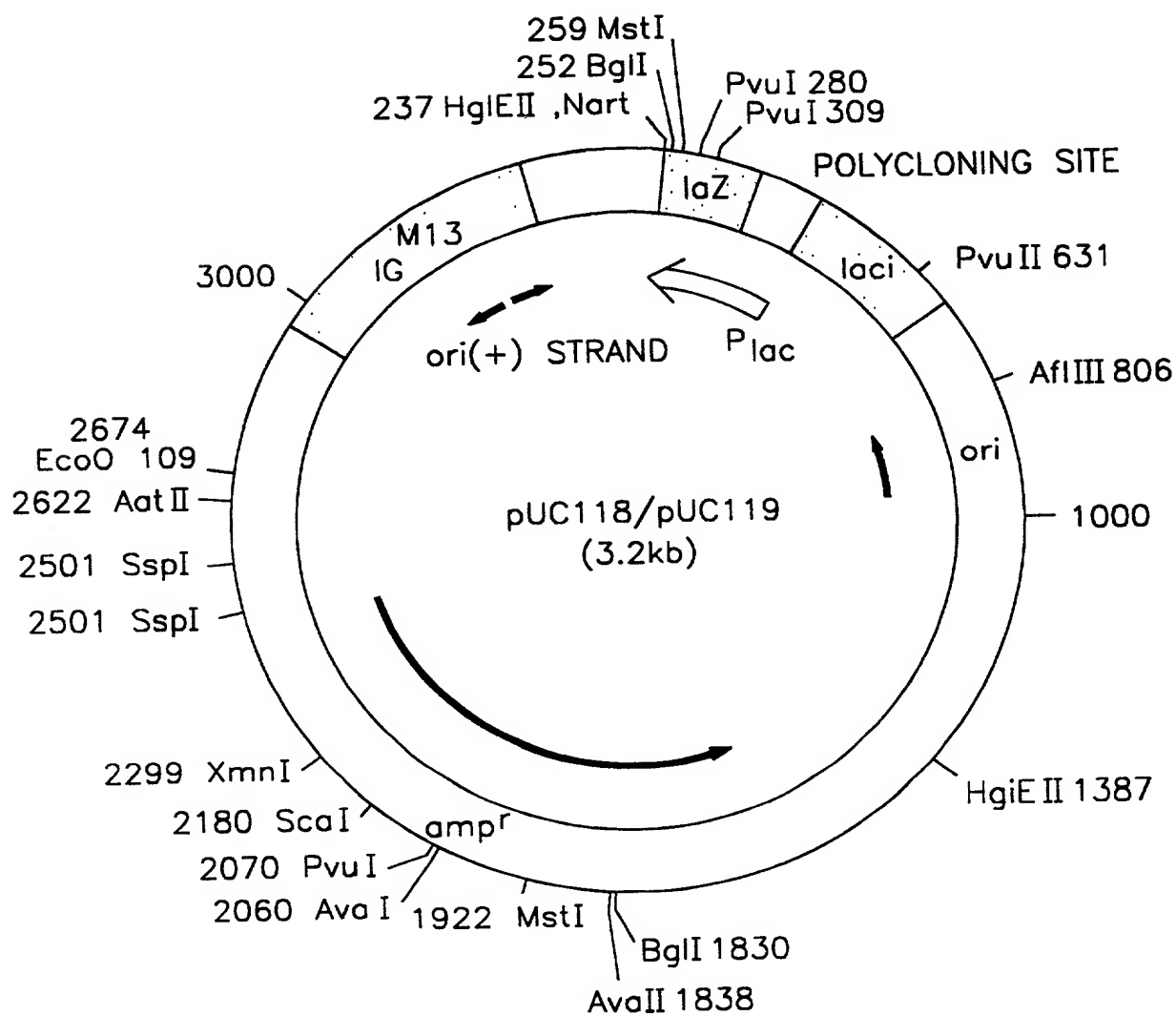


FIG. 5

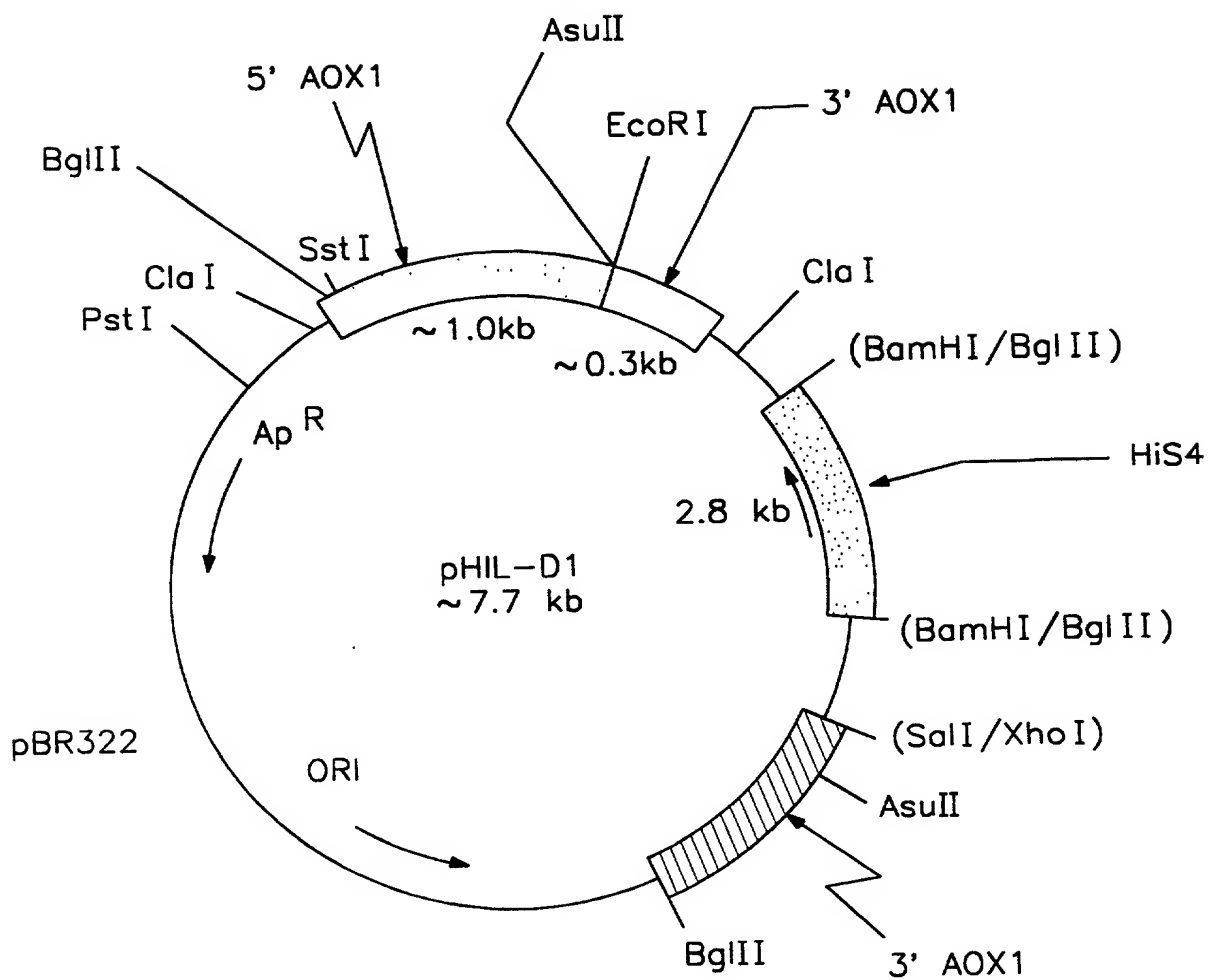


FIG. 6

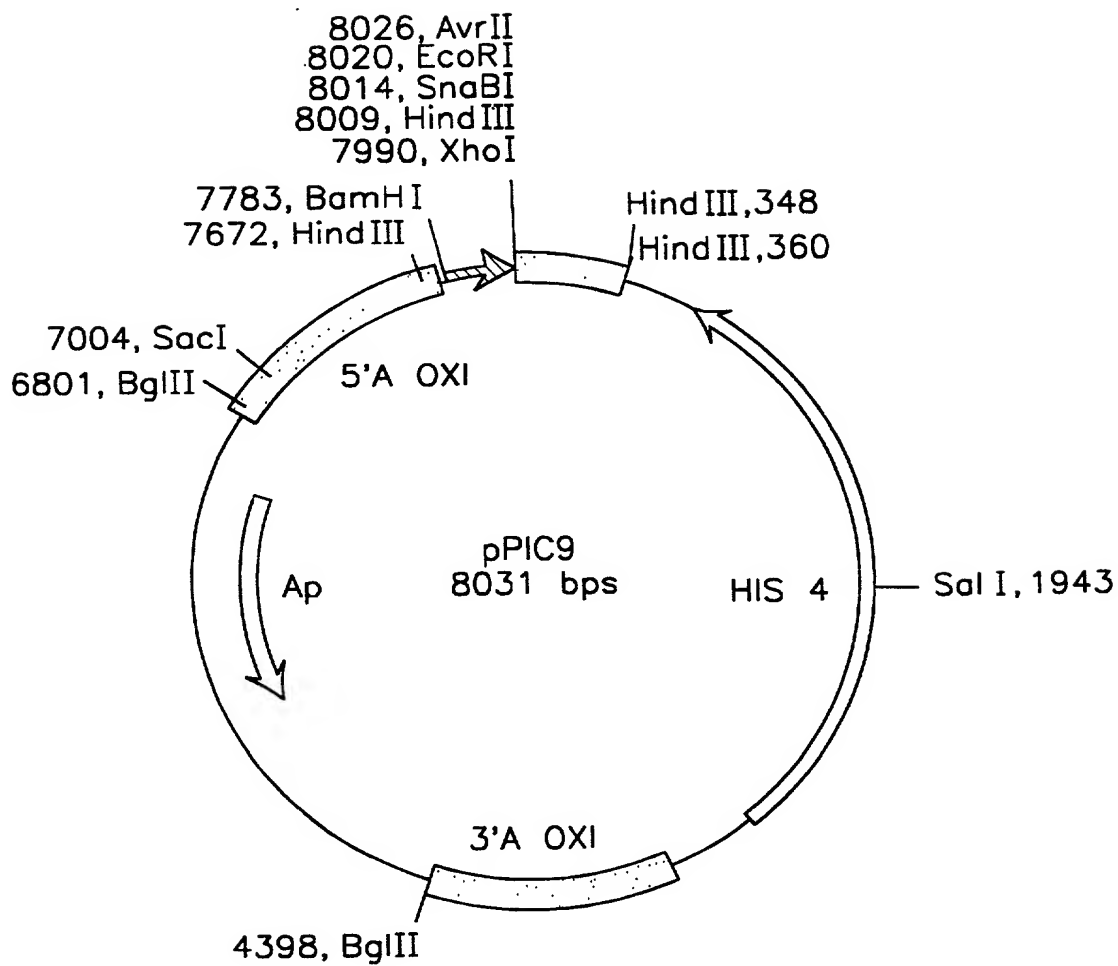


FIG. 7

1002096 1002096

BglI



HgiAI



Pvu II



Stu I

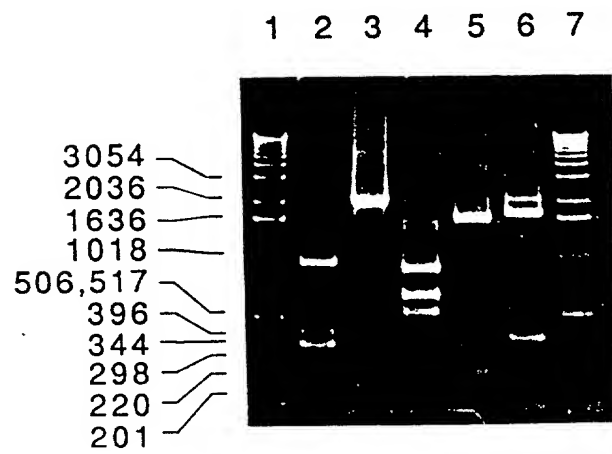


FIG. 8

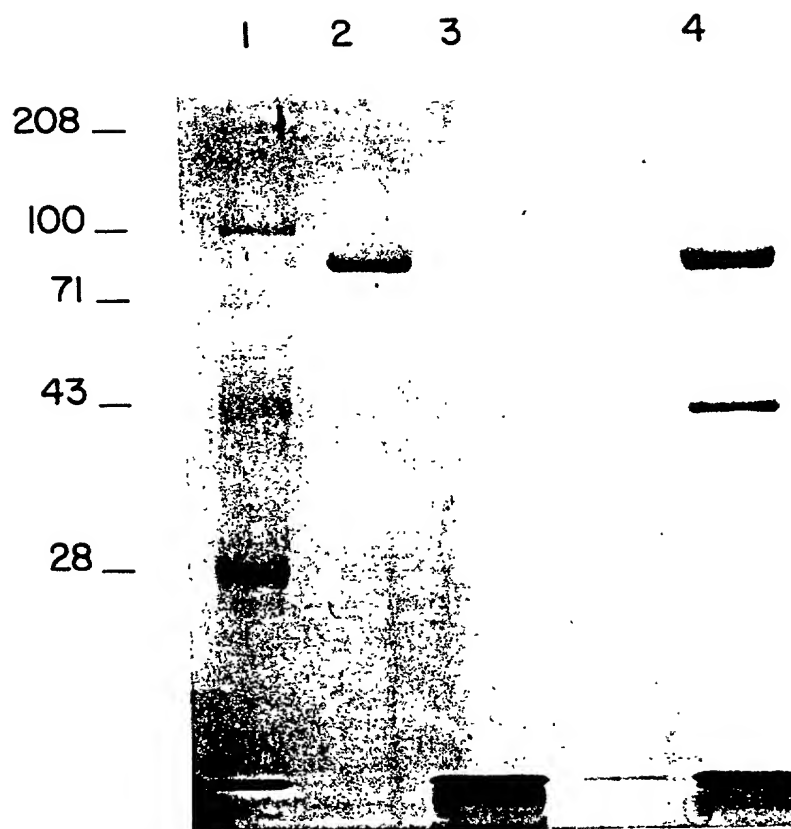


FIG. 9

1002006 43001

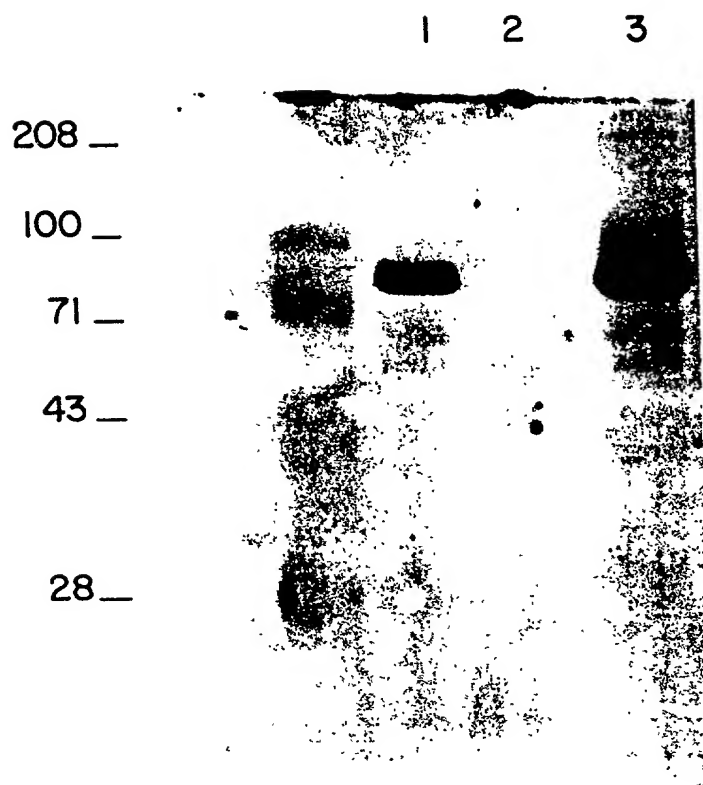


FIG. 10